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Figure 1a

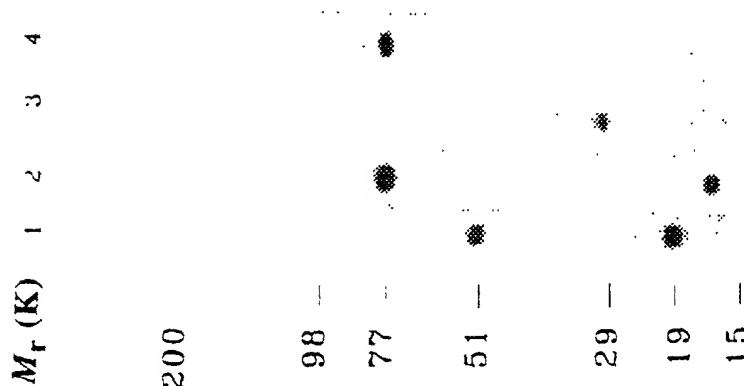
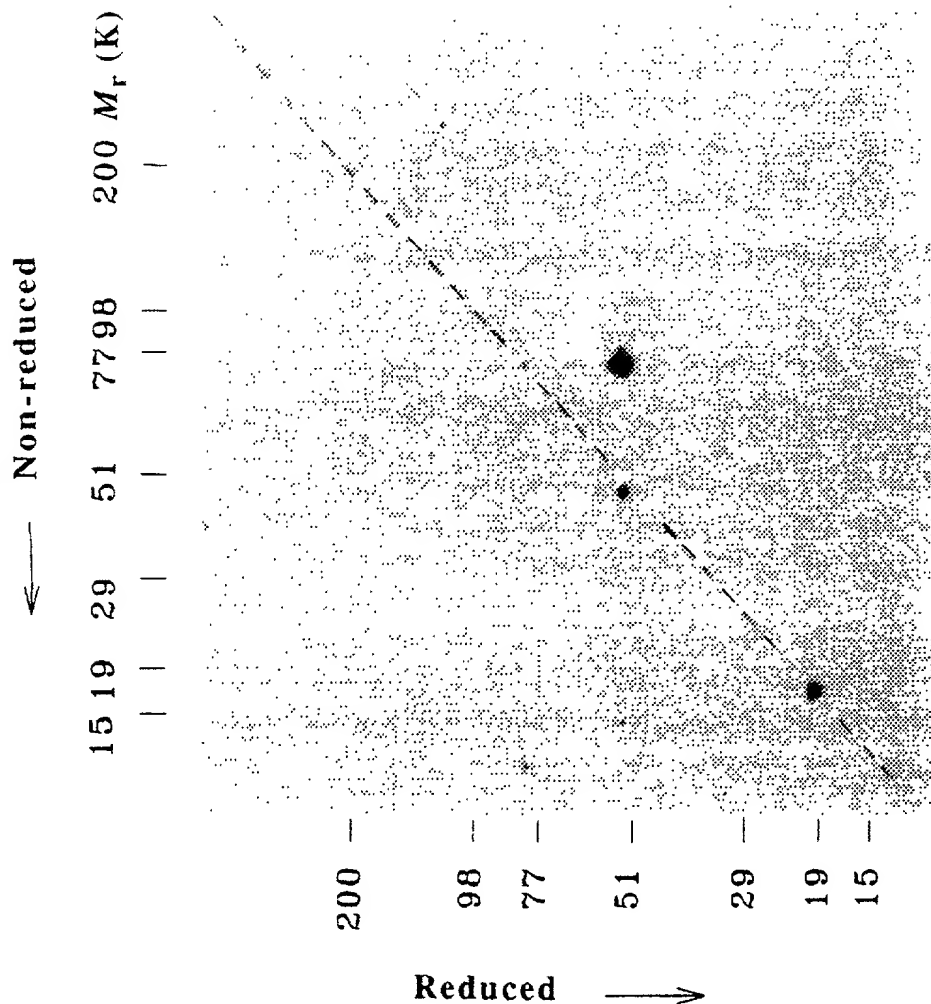


Figure 1b



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Figure 2

MASP-2	C1r/C1s → TPLGPKWPEPVFGRLASPGFPGEYANDOEERRWLTAPPGYRLRLYFTHFDLELSHLCEYDFVKLSSGAKVLATLGGQESTDTERAPGKDT			90
MASP-1	HTVELNNMFGQIQSPGYPDSYPSDSEVTWNITVPDGFRIKLYFMHFNLESSYLCEYDYVKVETEDQVLATFGRETDDTEQTPGQEV			87
C1r	SIPIPQKLFGVEVTSPLFPKYPNNFETTTTITVPTGYRVKLVFQQFDLEPSEGCFYDYVKISADKKSLGRFCGQLGSPGNPPGKKE			87
C1s	EPTMYGEILSPNYPQAYPSEVEKSWDIEVPEGYGIHLFYTHLDIELSENAYDSVQIISGDTTEGRLCGQRSSNNPHSPIVEE			83
	* * * * *			
MASP-2	FYSLGSSLDITFRSDYSNEKP FTGFEEAFYAEDIDEQ VAPGEA PTCDHHCHNHLGGFYCSCRAGYVLHRNKRTCSALCS			170
MASP-1	VLSFGSFMSTIFRSDFSNEER FTGFDHAYMAVDVDECK EREDEE LSCDHYCHNYIGGYECSRPGYILHTDNRTERVECS			167
C1r	FMSQGNKMLLTFTDSDSNEENGITIMFYKGLAYYQAVDLDEASRSKSGEEDPQCCQHLCHNYVGGYFCSERPGEYLEDHRSSQAECS			177
C1s	FQVPYNKLQVIFKSDFSNEER FTGFAAYVATDINECT DFVD VPCSHFCNNFIGGYFCSERPGEYFLHDDMKNEGVNCS			161
	* * * * *			
MASP-2	- C1r/C1s → GQVFTQRSSELSSPEYPRPYPKLSSCTYSISLEEGFSVILDFV ESFDVET HPETLCPYDFLKIQTDRREEHGPFCKGKTLPHR IETKS			256
MASP-1	DNLFTQRTGVITSPDPNPNPKSSECLYTIELEEGFMVNLFQF DIFDIED HPEVPCPYDYIKIKVGPKVLGPFCKGEKAPEP ISTQS			253
C1r	SELYTEASGYISSLEYPRSYPPDLRCNYSIRVERGLTLHLKFL EPFDIDD HQQVHCOPYDQLQIYANGKNIGEFCKGKQRPDP LDTSS			263
C1s	GDVFTALIGEIASPNYPKYPENSRCLEYQIRLEKGFQVVTLRREDFDVEAADSAGNC LDSLVFVAGDRQFGPYCKGHGFPGLNIETKS			250
	* * * * *			
MASP-2	CCP-1 → NTVTITFVTDESQDHTGKWIHYTSTAQCPYPMAPPN GHVSPVQAKYILKDSFSIFQETGYELLQGHLPKLSFTAVCKQKDGSDWRPMPA			345
MASP-1	HSVLILFHDNSNGENRGWRLSYRAAGNECPPELQPPVH GKIEPSQAKYFFKQDLVLSQDTGYKVLKDNVEMDTQIECLKDGTWSNKIPT			342
C1r	NAVDLLFTDESQDHRGWKLYRTTEIKQPPQKTLDEFTIIQNLQPOYQFRDYFIATCKOGYQLIEGNOVLHSFTAVCKDDGTWHRAMPR			353
C1s	NALDIIFQTDLTGQKKGWKLRYHGDPMPCPKEDTPN SVWEPAAKAKYVFRDVVQITELDGFVEVVEGRVGATSPYSTCKOSNGKWSNSKLG			338
	* * * * *			
MASP-2	CCP-2 → ESIVDCGPPDDLPSGRVEYITGPGVITYKAVIQYSCETPYTM KVNDDGYVCEADGFWTSSKGEKSLPVCEPVEGLS ARTT			426
MASP-1	CKIVDCRAPGELEHGLITFSTRNNLTYYKSEIKYSQEPYKML NNNTGIYTCQAQGVMMNKVLGRSLPTCLPVCGLPKFSRKL			426
C1r	CKIKDCGQPRNLPGDFRYTTTGMVNTYKARIQYQHEPYKMQTRAGSRESEQGVYTCQAQGIWKNEQKGEKIPRLPVCGLPKVPNPVEQ			443
C1s	CQPVDCGIPESIEGKVE DPESTLFGSVIRYTKHEPYIYME NGGGGEYHCKAGNSWVNEVLGPPELPPKVPVCGVPREPFE			419
	* * * * *			
MASP-2	serine protease → GGRIYGGQKAKPGDFPWQVLILGGTTA AGALLYDNWVLTAAH AVYEQKHDASALDIRMGTLLKRLSPHYTQAWSEAVFIHEG			507
MASP-1	MARIFNGRPAQKGTTPWIAMLSHLNGQPFCCGSLGSSWIVTAAHCLHQSLDPKDPDLRSDLLSPSD FKIIILGKHWRLRSDENEQHLG			515
C1r	RQRIIGGQKAKMGNFPWQVFTNIHGRG GGALLGDRWILTAAH TLYPKEHEAQSASLDVFLGHTNVEELMKLGNHP IRRV			523
C1s	KQRIIGGSDADIKNFPWQVFPDNPWA GGALINEYWVLTAAH VVEGNREPTMYVGSTSVQTSRLAKSKMLT PEHVFIHPG			498
	* * * * *			
MASP-2	YTHDAG FDNDIALIKLNKNVINSNITPICLPKEAESFMRTDDIGTAGWGLTQRGFLARNLMYVDIPVDHQQCTAAAYEK			589
MASP-1	VKHTTLHPKYDPNTFENDVALVELLESPVLNAFVMPICLP EGPQOEGAMVIVSGWGKQFLQRPPELTMEIEIPVDHSTQKAY			599
C1r	SVHPDYRQDESYN FEGDIALLELENSVTLGPNLLPICLP DNDTFYDLGLMGYVSGFGVMEEK IAHDLRFVRLPVPANPQACEN WLR			608
C1s	WKLLEV PEGRTN FDNDIALVRLKDPVKMGPTVSPICLPPTSSDYNLMDGLGLISGWGRTEKRDRAVLKAAKRLPVAPLAKCKEYKVE			586
	* * * * *			
MASP-2	PPYPRG SVTANMLCAGLESGGKDCRSGSGGALVFLDS ETERWVFGGIVSWGSMNCGEAGQYGVYTKVINYPWIENIISDF			671
MASP-1	APLKK KVRDMICAGEKEGGKDACSGDSGGPMVTLNR ERGQWYLVGTVSWG DCGKKDRYGVYSYIHNKDWIQRTVTVRN			680
C1r	GKNRMD VFSQNMFCAGHPSLQDQACQDSSGGVFAVRDP NTDRAWATGIVSWG GCSRG YGFYTKVLNLYVDWIKKEMEED			688
C1s	KPTADAEAYVFTPNMICAGGEK GMDSCCKGDSGGAFVQDPNDKTKFYAAGLVSWG CCGT YGLYTRVKYNYVDWIMKTMQENSTPRED			673
	* * * * *			

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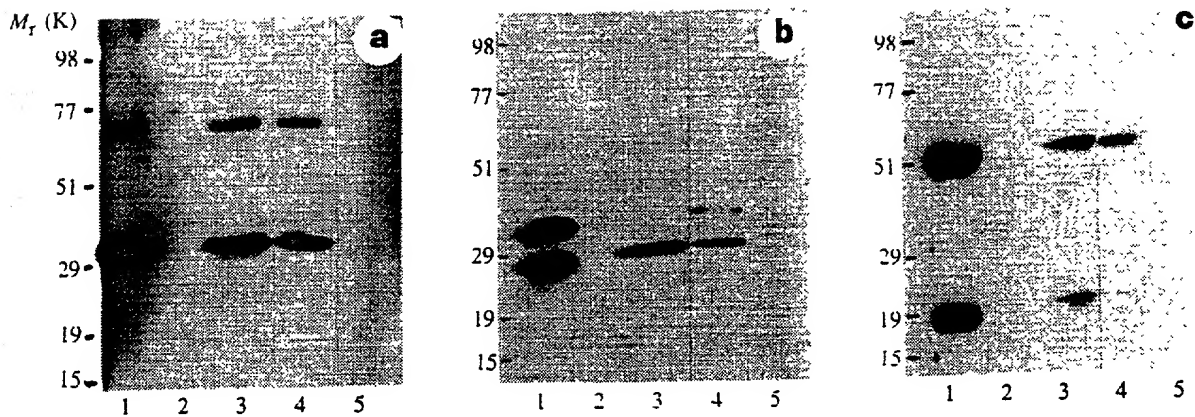
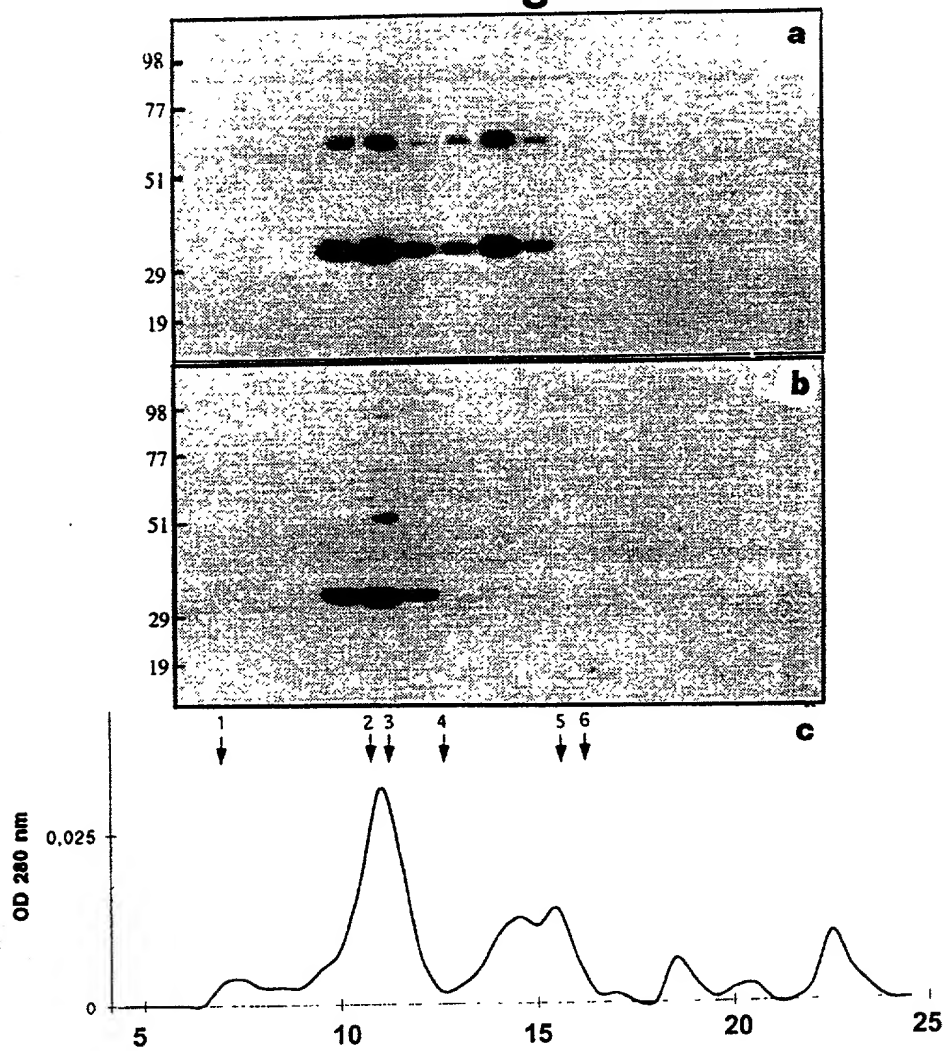


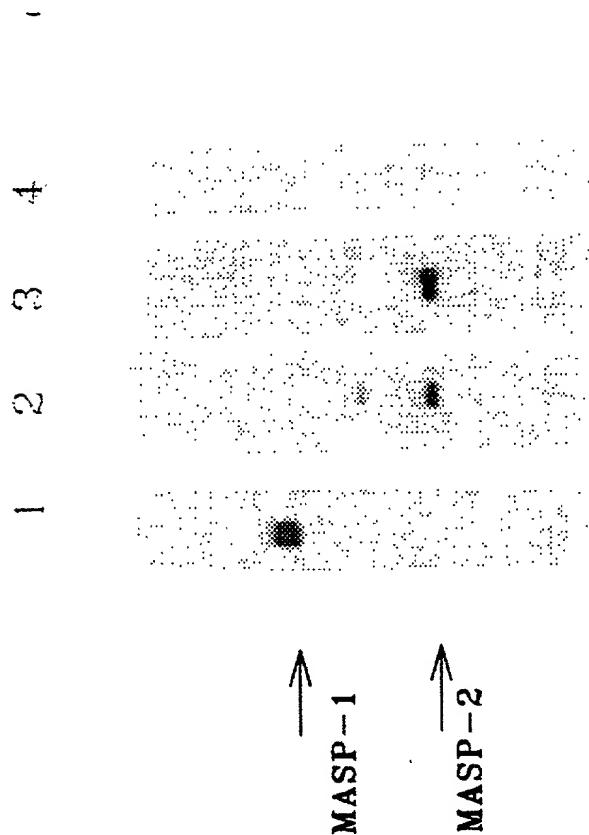
Figure 3b



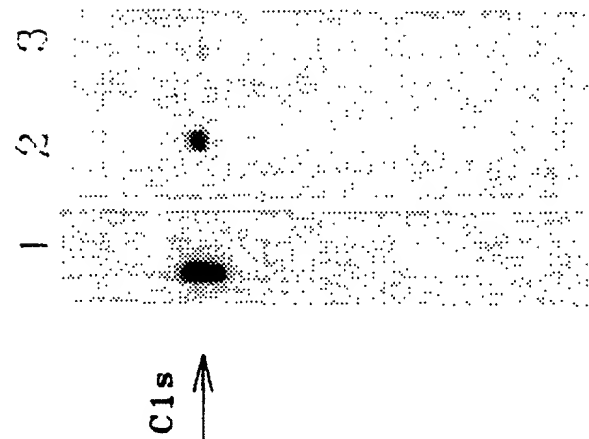
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Figure 4

Blot of MBL preparation

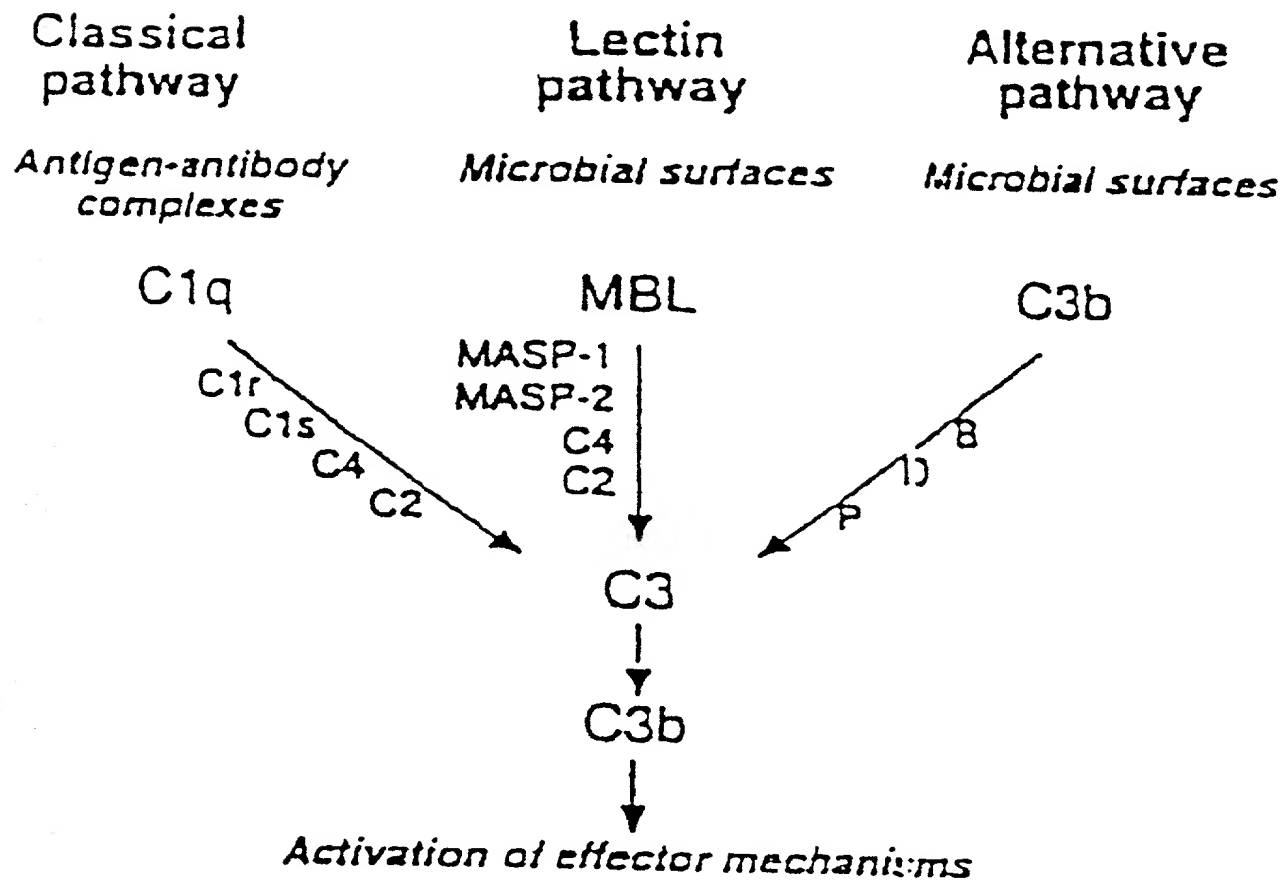


Blot of C1



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Figure 5



		+1
ctcgctgcatttcggcagcagggctggacggggcacacacatATGAGGCTGCTGACCCCTCCTGGGCTTCTGTGTGGCTCGGTGGCCACCCCTCTAGGCCCGAAGT	100	
<u>M R Y L T L L G L C L C G S Y A T P L G P K</u>	6	
GGCCTGAACCTGTGTTCCGGCGCCTGGCATCCCCCGGCTTTCACGGGGAGTATGCCATCACCAGGAGCGCGCTCGACCTGACTGCACCCCCCGGTA	200	
<u>W P E P V F G R L A S P G F P G E Y A N D Q E R R W T L T A P P G Y</u>	40	
CCGCTCGCGCTCTACTTCAACCCACTTCGACCTGGAGCTCTCCCACTCTGCGAGTACGACTTCGTCAAGCTGAGCTCGGGGGCCAGGTCTGGCCAG	300	
<u>R L R L Y F T H F D L E L S H L C E Y D F V K L S S G A K V L A T</u>	73	
CTGTGCGCGCAGGAGAGCACACACCGAGCGGGCCCTGGCAAGGACACITTTCTACTCGCTGGGCTCCGCTCGGACATTACCTTCCGCTCCGACTACT	400	
<u>L C Q E S T T D T E R A P G K D T F Y S L G S S L D I T F R S D Y</u>	106	
CCAACGAGAAGCCGTTTACGGGCTTCGAGGCTTCATATCAGCCAGGACATTGACGAGTCCAGGTGGTCCCGGAGAGCGCCCACTCGGACACCA	500	
<u>S N E K P P T T G F E A F Y A A E D I D E C Q V J P G E A P T C D H H</u>	140	
CCACACCACTGGGCGGTTTCTACTGCTCCTGCGCGCAGGCTACGTCCTGCACGTAACAGCGCACCTGCTCAGCCCTGTGCTCCGGCCAGGTC	600	
<u>C H N H L G G F Y C S C R A G Y V L H R N K R T C S A L C S G Q V</u>	173	
TTACCCAGAGGCTCTGGGAGCTCAGCAGCCCTGAATACCACGGCCGTATCCCAACTCTCCAGTTGCACTTACAGCATCAGCCTGGAGGAGGGTTCA	700	
<u>F T Q R S G E L S S P E Y P R P Y P K L S S C T Y S I S L E E G F</u>	206	
GTGTCACTCTGGACTTTGTGGAGTCTTCGATGTGGAGACACACCTGAAACCTCTGCTCCCTACGACTTCTCAAGATTCAACAGACAGAGAGAACA	800	
<u>S V I L D F V G E S F D V E T H P E T T L C P Y D L K I Q T D R E E H</u>	240	
TGGCCCATTTCTGTGGGAAGACATTGCCCCACAGGATTGAAACAAAAGCAACCGTGACCATCACTTTGTGTCACAGTGAATCAGGAGACCACACAGGC	900	
<u>G P F C G K T L P H R I E T K S N T V T I T F V T D E S G D H T C</u>	273	
TGGAAGATCCACTACAGGACACAGCGCAGCCTTGCCCTTATCCGATGGCGCCACCTAATGGCCACGTTTCACCTGTGCAAGCCAAATACATCTCGAAG	1000	
<u>W K I H Y T T S T A Q P C P Y P M A P P N G H V S P V Q A K Y I L K</u>	306	
ACAGCTTCTCCATCTTTGCGAGACTGGCTATGAGCTTCTGCAAGGTCACTTCCCCCTGAAATCTTTATGCAAGTTCAGAAAGATGGATCTTGGGA	1100	
<u>D S F S I F C E T G Y E L L Q G H L P L K S F T A V T C Q K D G S W D</u>	340	
CCGCCCCAATGCCCGCTGCGACATTGTTGACTGTGGCTCTCGATGATCTACCCAGTGGCCGAGTGGATACATCACAGGTCCTGGAGTGACCACTAC	1200	
<u>R P M P A C S I V D C G P P D D L C P S G R V E Y I T G P G V T T Y</u>	373	
AAAGCTGTGATTCACTACAGCTGTGAAGAGACCTTCTACACAATGAAAGTGAATGATGTTAATATGTTGTGTAGCGCTGATGGATTCTGGACGAGCTCCA	1300	
<u>X A V I Q Y S C E E T F Y T M K V N D G K Y V C E A D G F W T S S</u>	406	
AAGGAGAAAAATCACTCCAGTCTGTGAGCCTGTTTGTGACTATCAGCCCGCAACAAGGAGGGGCTTATATGGAGGGCAAAAGGCAAAACCTGGTGA	1400	
<u>K G E K S L P V C E P V C G L S A R T T G G R I Y G G Q K A K P G D</u>	440	
TTTTCTTGGCAAGTCTGATATTAGGTGGAACACAGCAGCAGGTGCACTTTATATGACACTGGGTCTTAACAGCTGCTGCGCTCTATGAGCAA	1500	
<u>F P W Q V L I L G G T T A A G A L L Y D N W L T A C H A V Y E Q</u>	473	
AACATGATGCATCCGCCCTGGACATTGGAATGGGCAACCTGAAAGACTATCACCTATTATACACAGCCTGGTCTGAAGCTGTTTATATCATGAAG	1600	
<u>A H D A S A L D I R M G T L K R L S P H Y T Q A W S E A V F I H E</u>	506	
GTTATATCATGATGCTGGCTTTGACAATGACATAGCACTGATTAAATTGAATAACAAAGTTGTAATCTATAGCAACATCAGCCCTATTTGCTGCCAAG	1700	
<u>G Y T H D A G F D N I A L I K L N N K V V I N S N I T P I C L P R</u>	540	
AAAAGAAAGCTCAATCTTTTAGGACAGATGACATGGAACTGCACTCTGGATCGGGATTAACCCAAAGGGGTTTCTTGCTAGAAATCTAATGTATGTC	1800	
<u>K E A E S F M R T D I G T A S G W G L T Q R H F L A R N L M Y V</u>	573	
GACATACCGATTGTTGACCATCAAAAATGTACTGCTGCATATGAAAAGCCACCTATCCAGCGGGAAGGTAACTGCTAACATGCTTTGTGCTGGCTTAG	1900	
<u>D I P I V D H Q K C T A A Y E K P P Y P R G S V T A N M L C A G L</u>	606	
AAAGTGGGGCAAGGACAGCTGCAGAGGTGACAGCGGAGGGGCACTGGTGTCTAGATAGTGAACAAGAGGTGGTTTGTGGGACCAATAGTGTCTGT	2000	
<u>E S G G K D S C R G D G G A L V F L D S E T E R W F V G G I V S W</u>	640	
GGGTTCCATGAATTGTGGGGAAGCAGGTCACTATGGAGTCTACACAAAGTTATTAACATATCCCTCGATCGAAGACATAATTAGTGATTTTAACTT	2100	
<u>G S H N C G E A A G G T Y G V Y T K V I N Y I P A I E N I I S D F A T O P</u>	671	
gcgtgttcgaagtcaggattcttccatttttagaataatgcctgtggaagacctctggcagcgagctggcttcgagaagcattccatcattactgtggacatggca	2200	
<u>ctgtctgtcccccaccccccaaaaacagactccaggctgcgtgcctcttccactctgcaggttttaactccagccttccccattgactcaagggggacat</u>	2300	
<u>aaacacagagatgtgacagctcattcttggccacccactgtcaatgtcactgtctcaaaccttcaattcaattcaattcaattcaattcaattcaattcaatt</u>	2400	
<u>ctggcagctctgttaaaactgtcgtctccatctgtctcttctttaaactgtctcttcttaactcaaaaaa</u>	2475	